

FIGURE 2A.

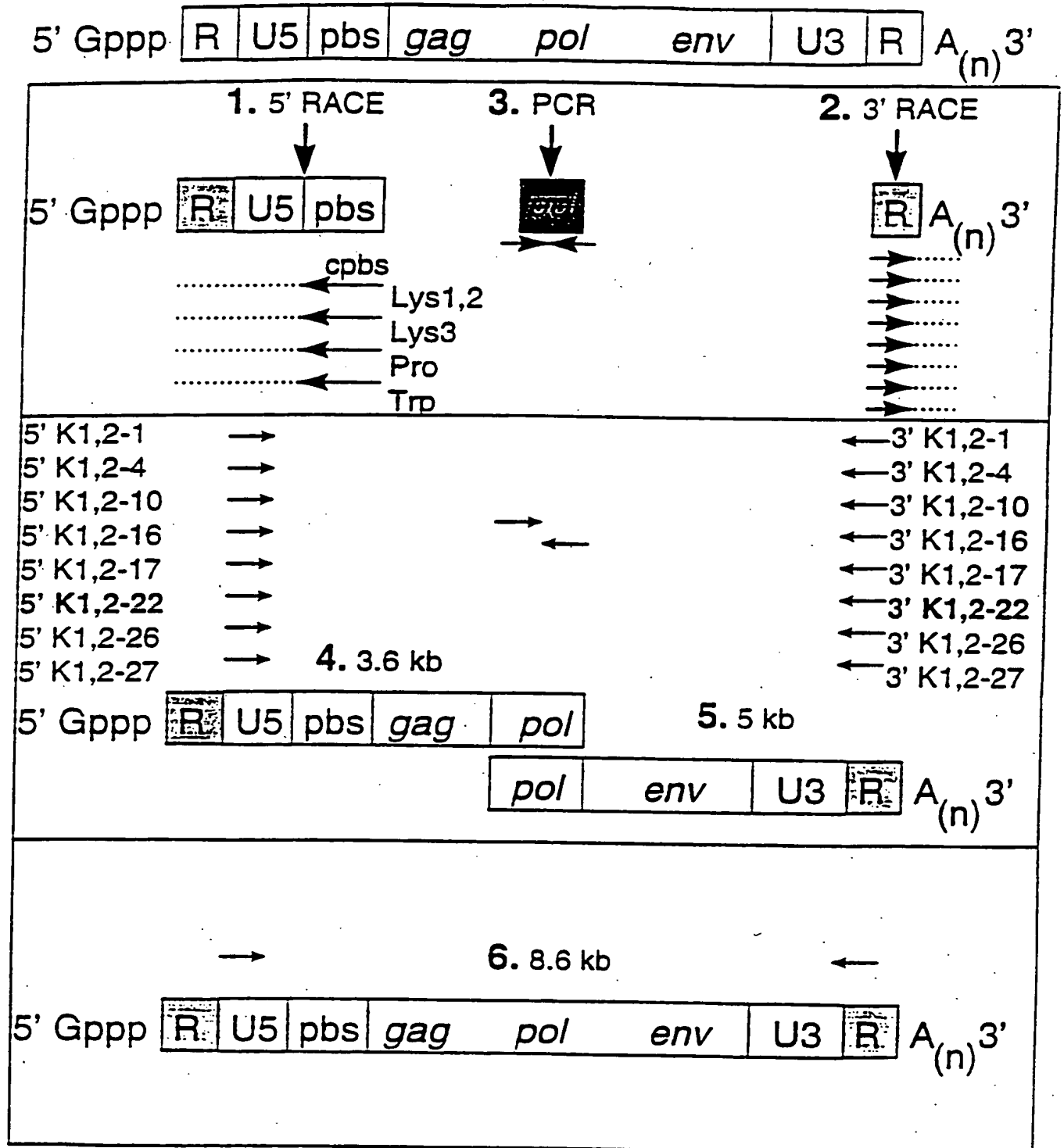
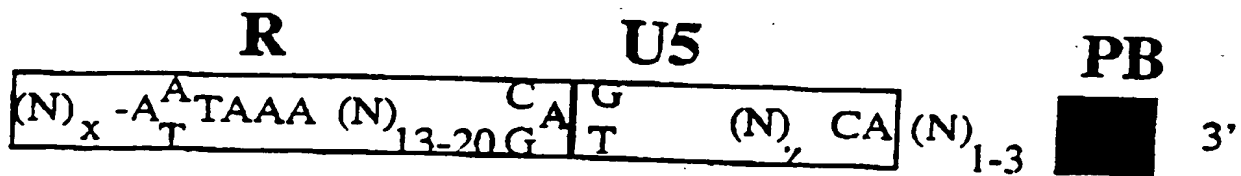


FIGURE 2B



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FIGURE 2C

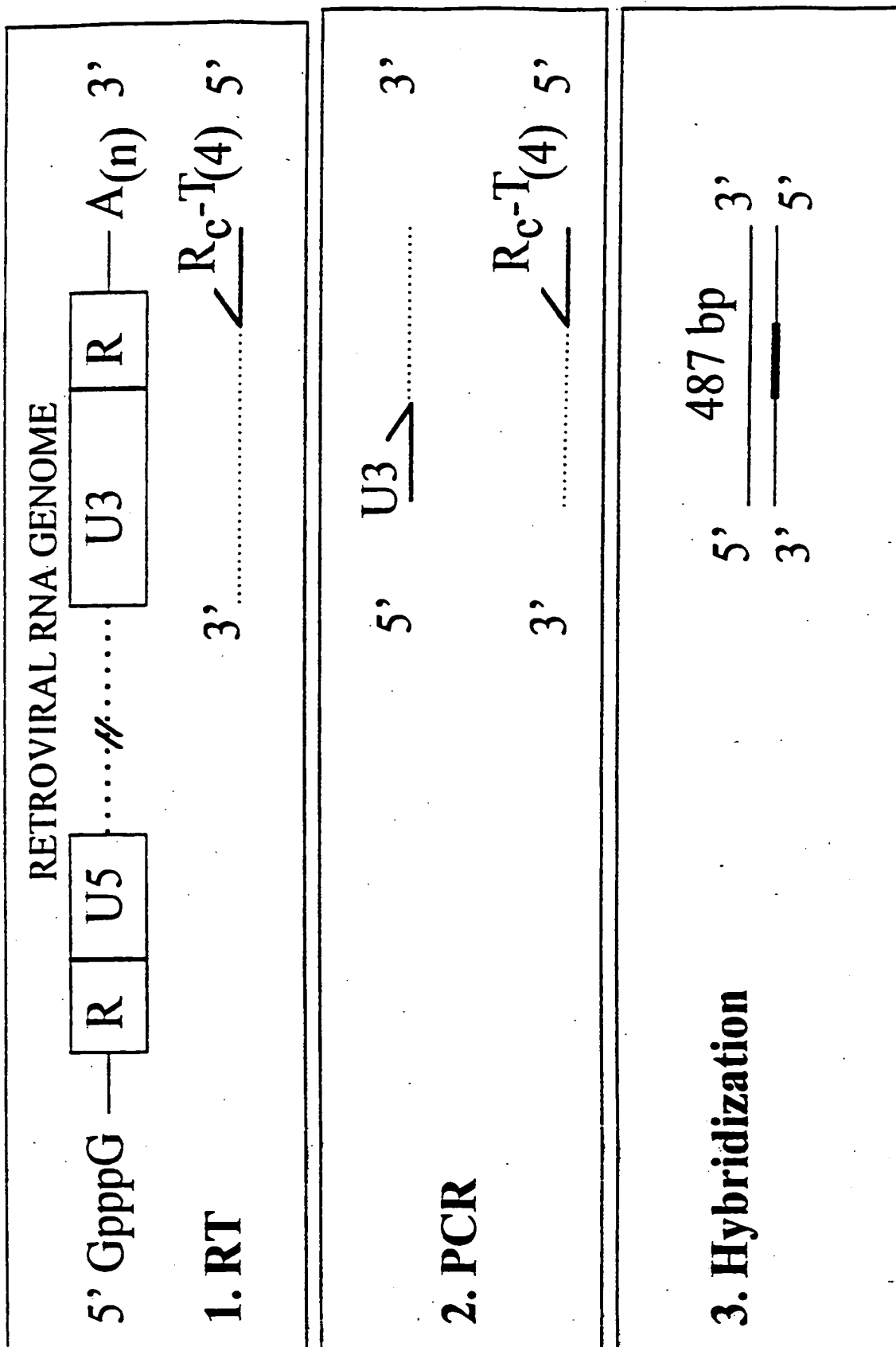


FIGURE 2D

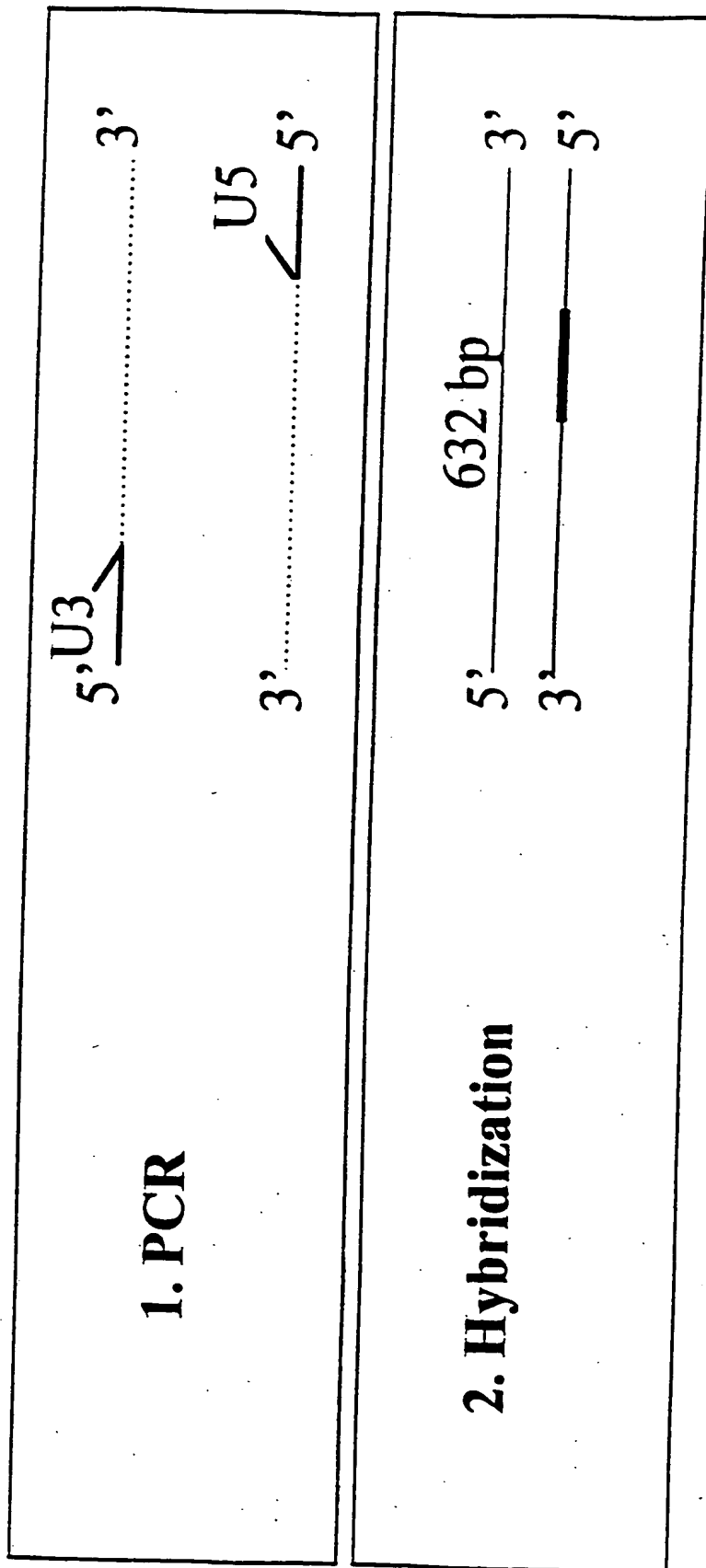
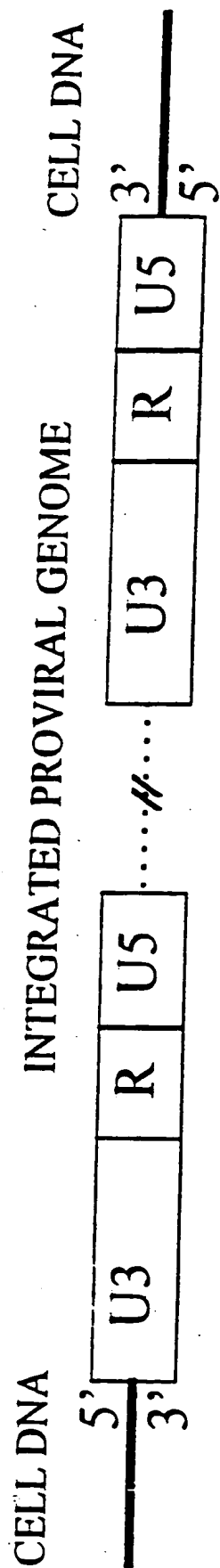


FIGURE 2E

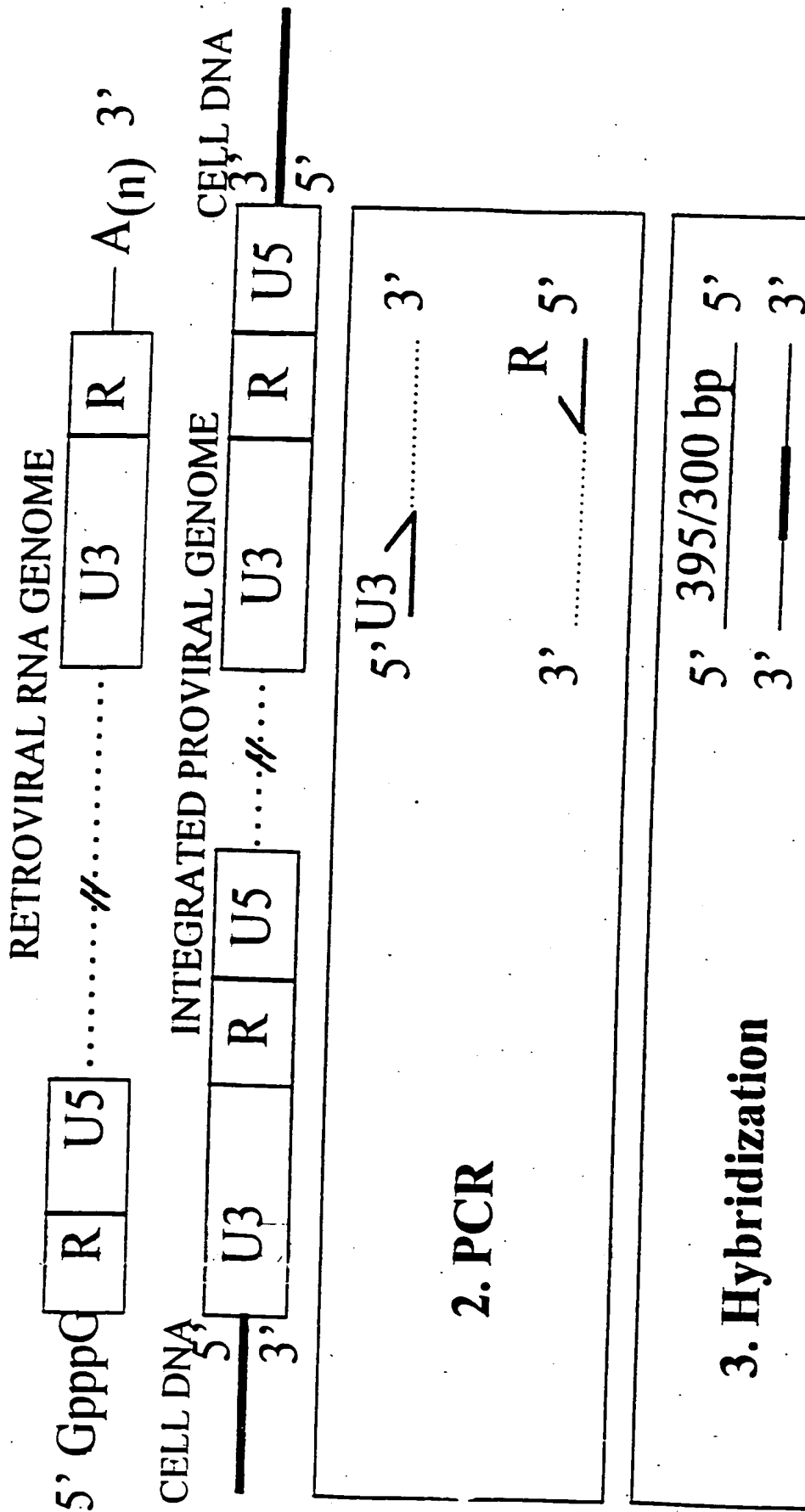


FIGURE 2F











TEMPLATE	SPECIFICITY	IDDM PATIENTS (n=10)	CONTROLS (n=10)
RNA	RT+ U3-R		
	RT+ U3-R-POLY(A)		
	RT- U3-R		
	RT- U3-R-POLY(A)		
DNA			

FIGURE 3A.

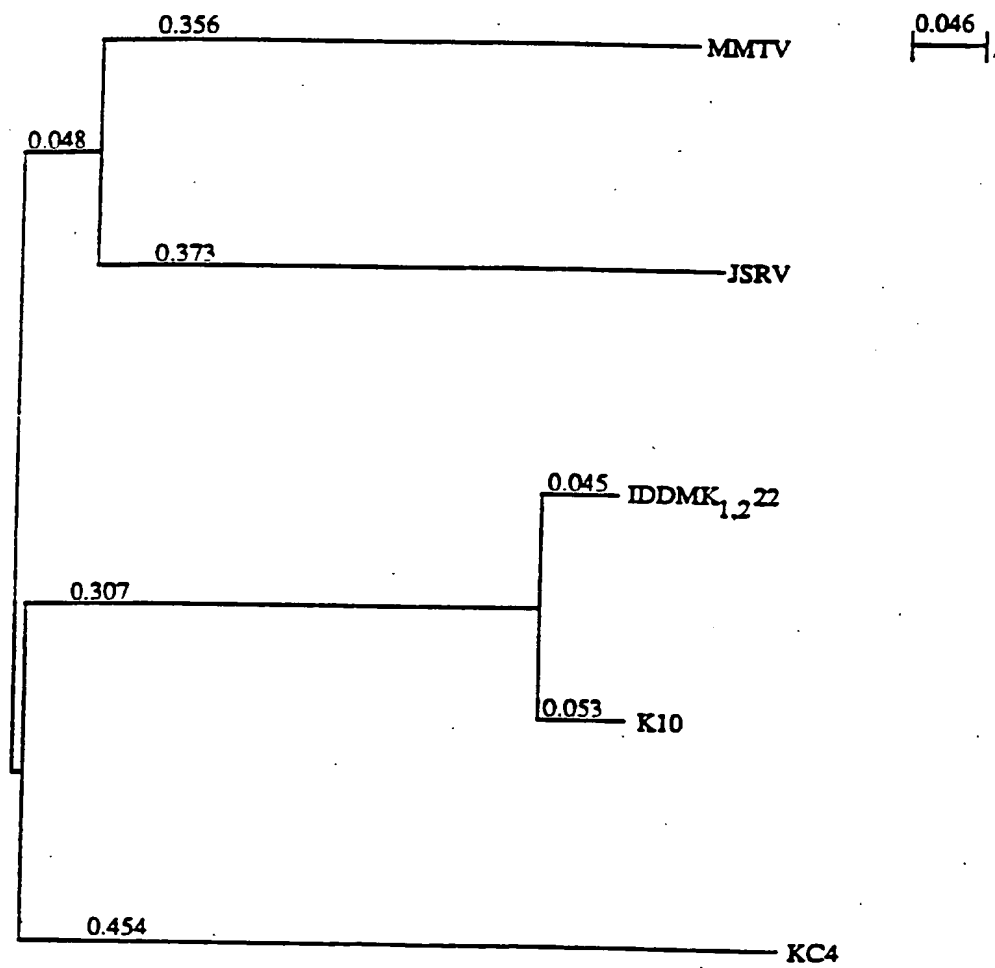


FIGURE 3B.

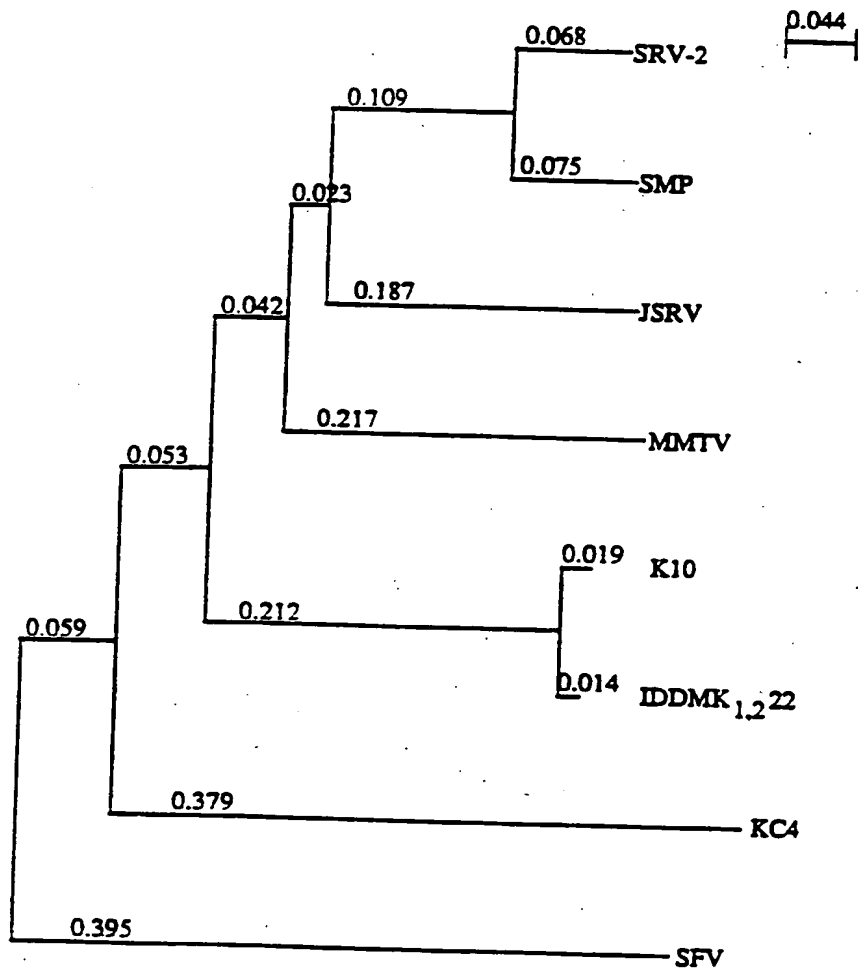


FIGURE 3C.

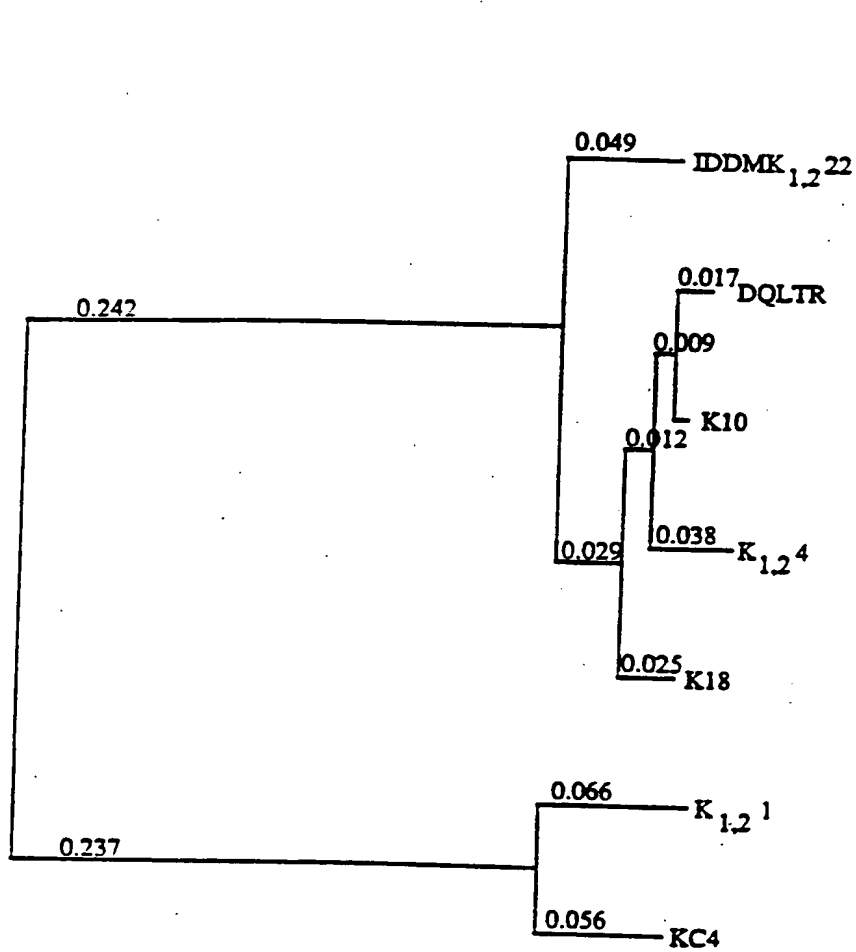


FIGURE 4A.

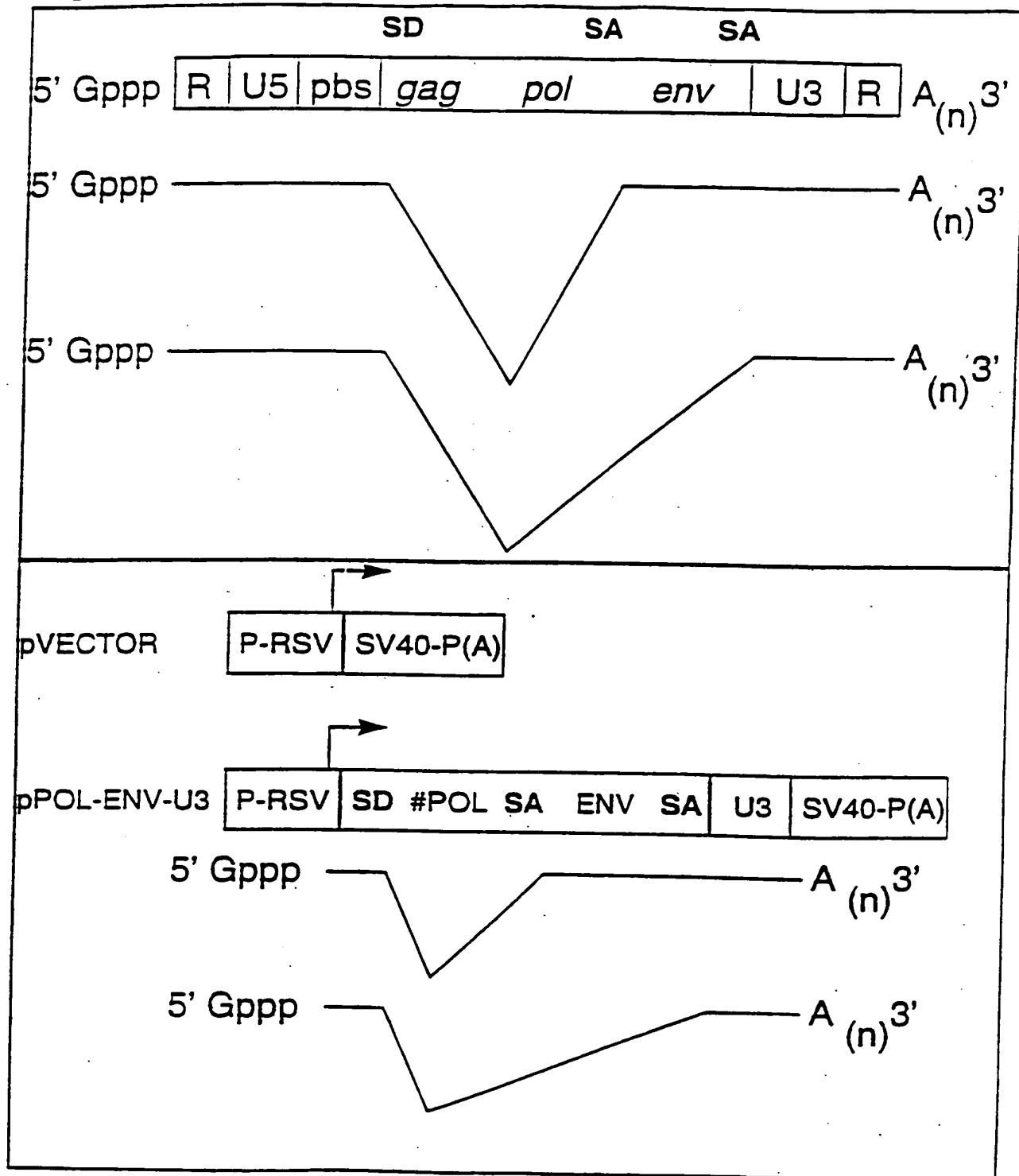


FIGURE 4B.

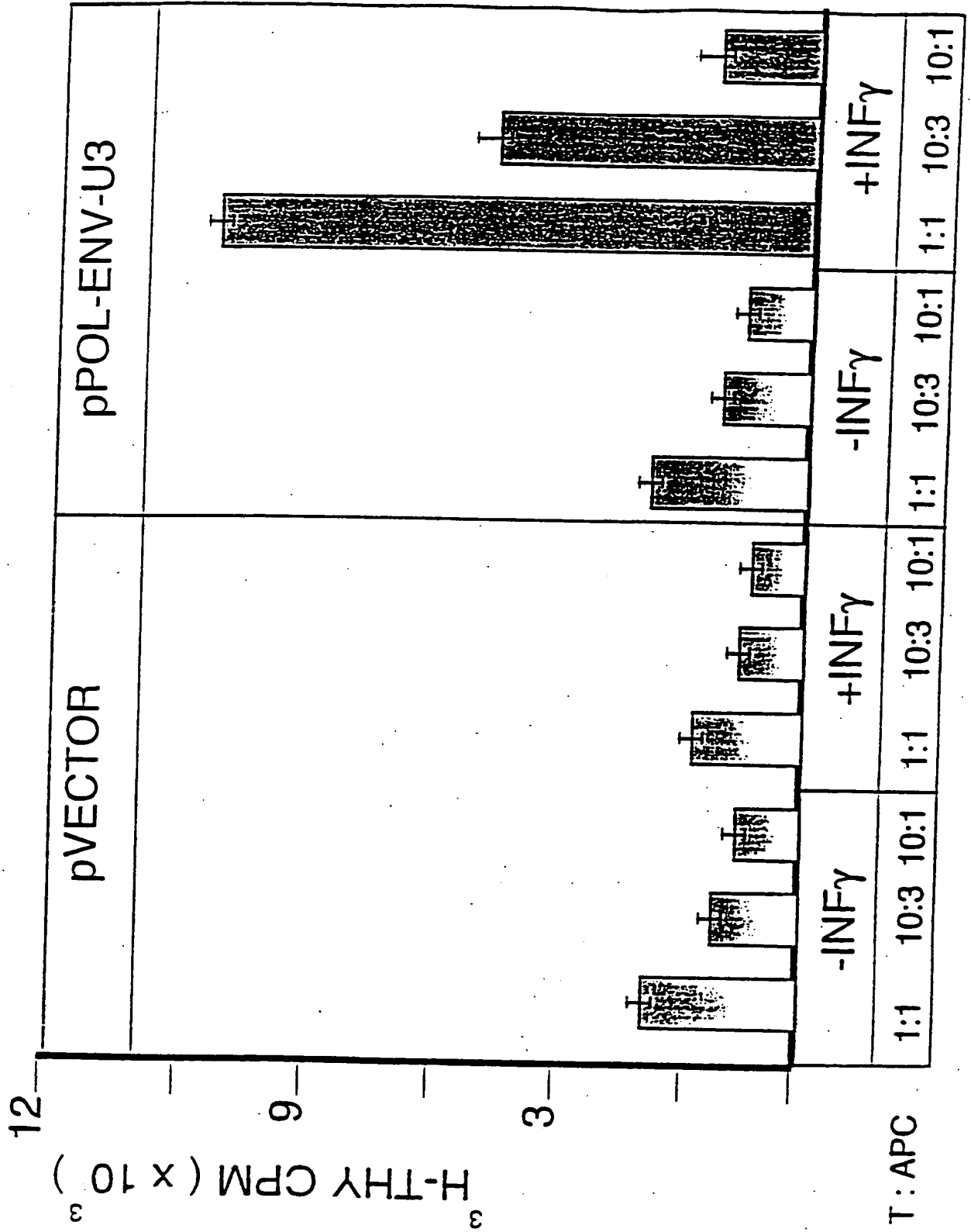
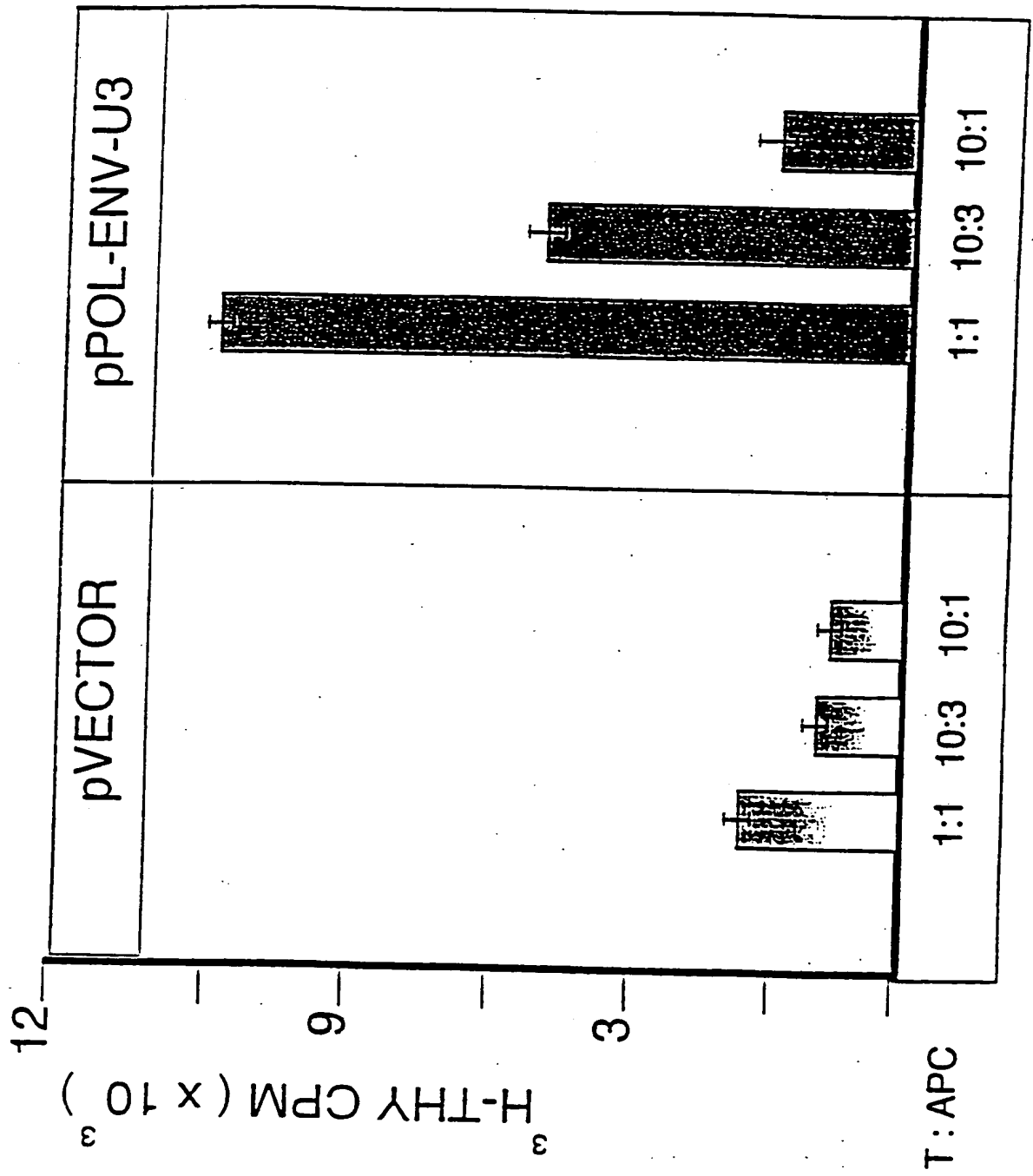


FIGURE 4C.



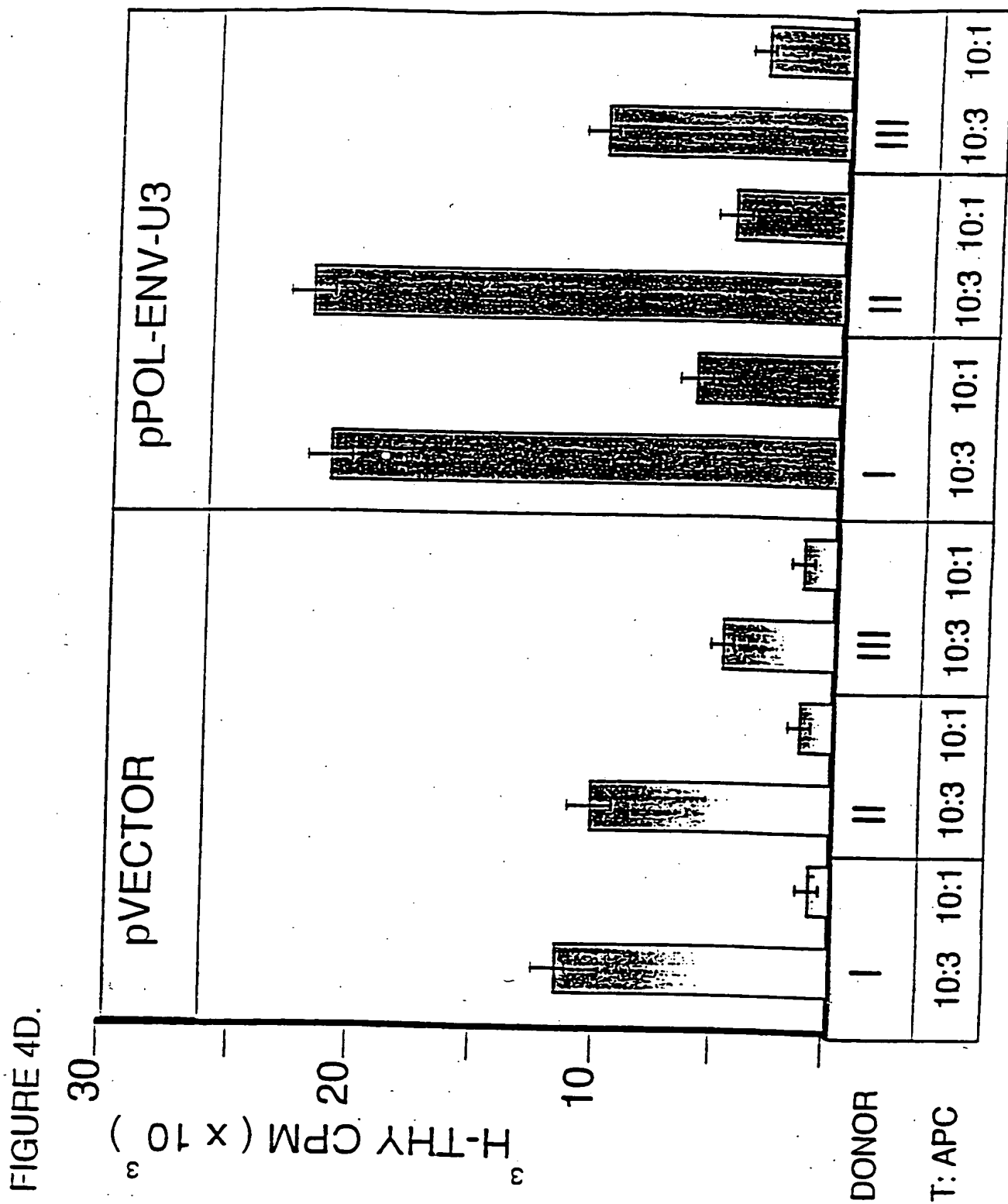


FIGURE 5.

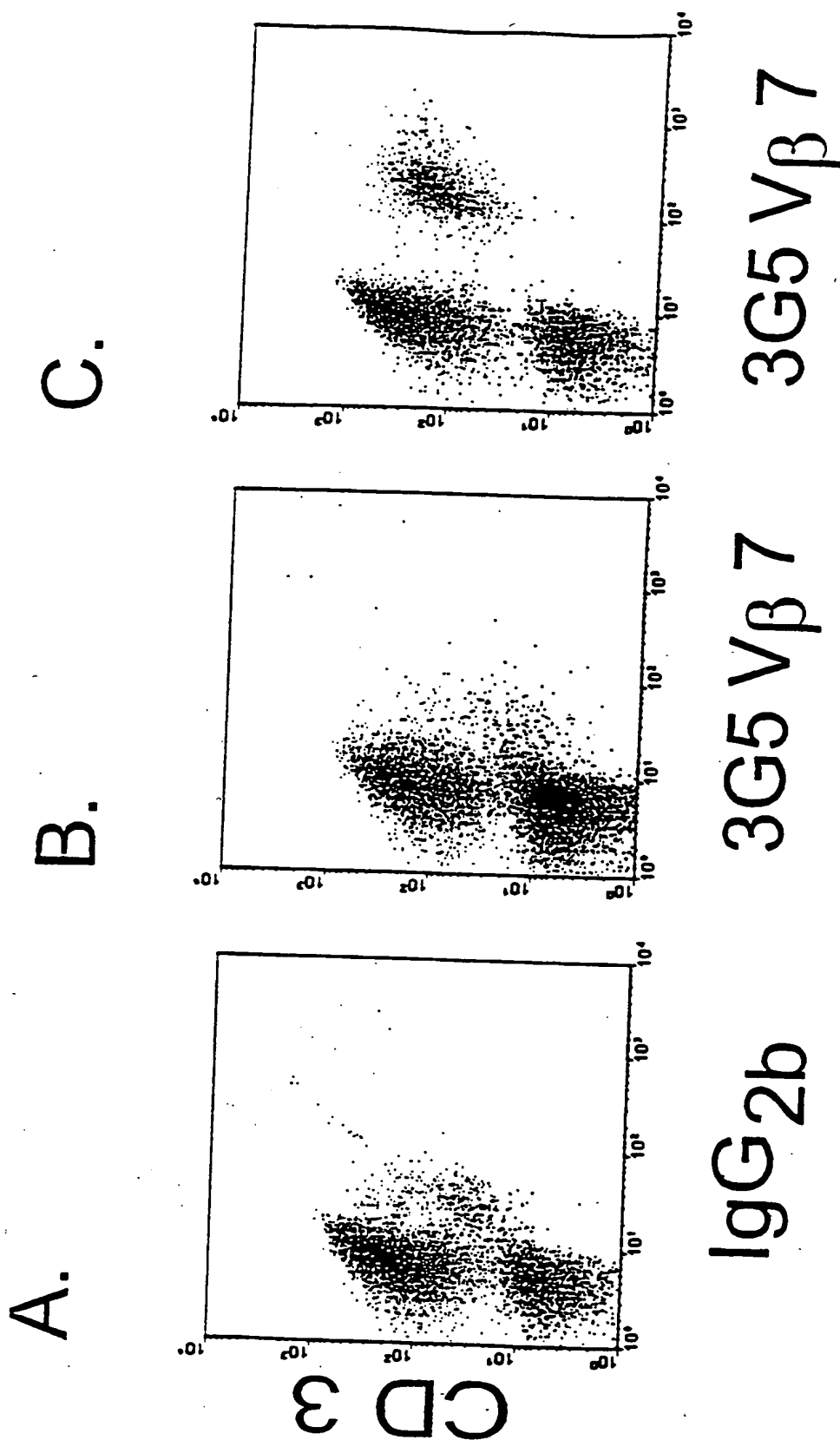


FIGURE 6A.

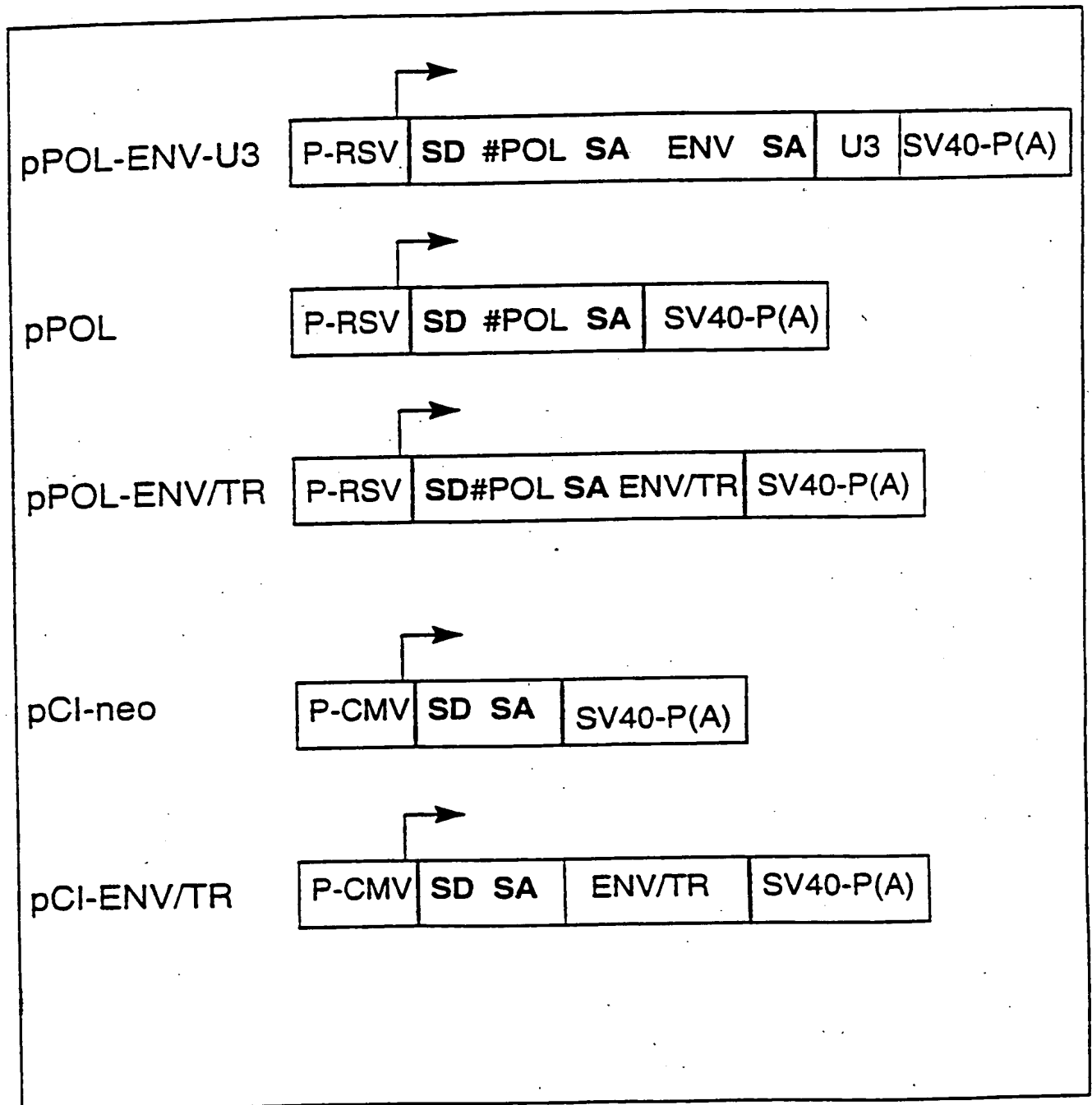


FIGURE 6B.

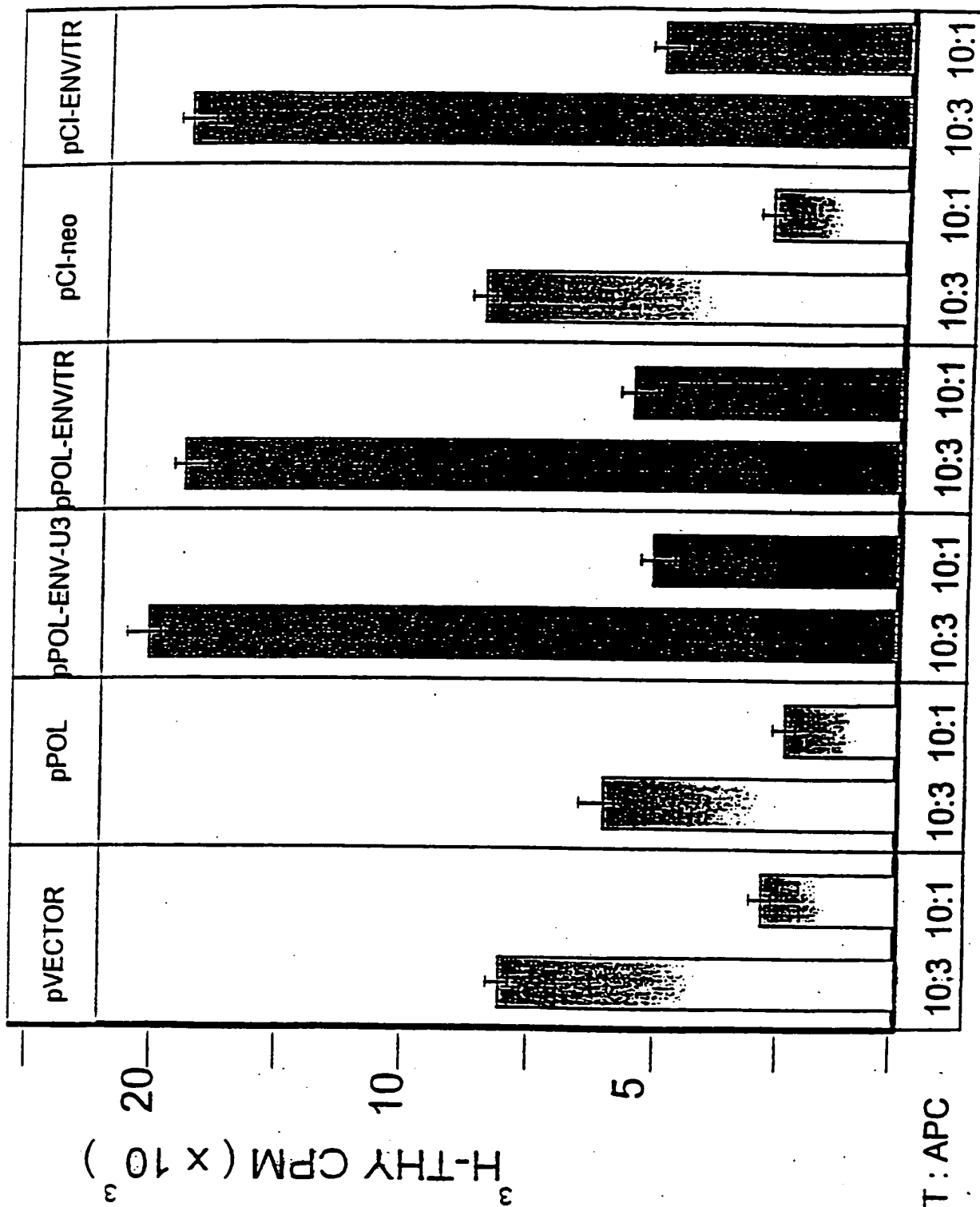


FIGURE 7A

iddmk1,2 22-5'1tr

CATCTCCCTCAGGAGAAACACCCACGAATGATCAATAAATACTAAGGGGACTCAGAGGCTGGT
GGGATCCTCCATATGCTGAACGTTGGTTCCCGGGGCCCCCTTATTTCTTTCTCTATACTTTGT
CTCTGTGTCTTTTTCTTTTCCAAGTCTTCTTCATTTGCACCTTACGAGAAACATCTCCATCAT
GGTTGTTGGATGGGGGCAA

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FIGURE 7B

iddmk1,2 22-3'ltr

CTGCAGGTGTACCCAACAGCTCCGAAGAGACAGTGACATCGAGAACGGGGCCATGATGACGATG
GCGGTTTTGTGCGAAAAGAAAAGGGGGAAATGTGGGGAAAAGCAAGAGAGATGAGATTGTTACT
GTGTCTGTATAGAAAGAAGTAGACATAGGAGACTCCATTTTGTTCTGTACTAAGAAAAATTCT
TCTGCCTTGAGATGCTGTTAATCTATGACCTTACCCCCAACCCCGTGCTCTCTGAAACATGTG
CCGTGTCAAACTCAGGGTTAAATGGATTAAGGGTGGTGCAAGATGTGCTTTGTTAAACAGATG
CTTGAAGGCAGCATGCTCATTAAGAGTCATCACCACTCCCTAATCTCAAGTACCCAGGGACAC
AAACACTGCGAAAGGCCGCGAGGGACCTCTGCCTAGGAAAGCCAGGTATTGTCCAAGGTTTCTC
CCCATGTGATAGTCTGAAATATGGCCTCGTGGGAAGGGAAAGACCTGACCATCCCCCAGACCA
ACACCCGTAAAGGGTCTGTGCTGAGGAGGATTAGTATAAGAGGAAAGCATGCCTCTTGCAAGTT
GAGAGAAGAGGAAGACATCTGTCTCCTGCCCATCCCCGTTGGGCAATGGAATGTCTCAGTATAAA
ACCCGATTGAACATTCCATCTACTGAGATAGGGAAAAACTGCCTTAGGGCTGGAGGTGGGACA
TGTGGGCAGCAATACTGCTTTGTAAAGCATTGAGATGTTTATGTGTATGTATATCTAAAAGCA
CAGCACTTGATCCTTTACCTTGTCTATGATGCAAACACCTTTGTTACAGTGTTTGTCTGCTGA
CCCTCTCCCCACTATTGTCTTGTGACCCTGACACATCTCCCTCAGGAGAAACACCCAcgaatg
atcaataaataactaaggggactcagaggctggtgggatcctccatattgctgaacggttggttcc
cggggcccccttatttctttctctatactttgtctctgtgtctttttctttttccaagtcttct
tcatttgcaccttacgagaaacatctccatcatgggttggttgatgggggcaa

FIGURE 7C

iddmk1,2 22-env

ATGGTAACACCAGTCAATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGG
 GTACCTGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAAT
 ATTTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTAATGCCT
 GCAGTCCAAAATTGGTTGGTAGAAGTACCTACTGTCACTCCTAACAGTAGATTCACTTATCAC
 ATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGA
 TCATTAAAATTTAGACCTAAAGGGAAAACTTGCCCCAAGGAAATTCCTAAAGGATCAAAGAAT
 ACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAA
 TTCGGAATATTATAGATTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACT
 CAGTCGTGTCCAAGTGCAAGTGAGTCCAGCTGTGATAGCGACTTAACAGAAAGTCTAGAC
 AAACATAAGCATAAAAAATTACAGTCTTTCTACCTTTGGGAATGGGAAGAAAAAGGAATCTCT
 ACCCCAAGACCAAAAAATAAGTCTGTTTCTGGTCTGGAACATCCAGAATTGTGGAGGCTT
 AAGCCATTTTATACCTATCGACCTAAATTCATTCTAACGGTTCCCTTACAAAGTTGCCTAAAG
 CCCCCTTATATGCTAGTTGTAGGAAATATAGTTATTAACCAGCCTCCCAAATATAACCTGT
 GAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAGCACCGTATTCTGCTG
 GTGAGAGCAAGAGAAGGCATGTGGATCCCTGTGTCCACGGACCGGACCGTGGGAGGCCTCGCCA
 TCCATCCATATTTTGAAGTAAATATTAAGGCGTTTAAATAGATCCAAAAGATTCAATTTT
 ACTTTAATTGCAGTGATTATGGGATTAATTGCAGTCACAGCTACGGCTGCTGTGGCAGGGGTT
 GCATTGCACTCTTCTGTTCACTCAGTAAACTTTGTTAATTATTGGCAAAGAATTCTACAAGA
 TTGTGGAATTCACAATCTAGTATTGATCAAAAATTGGCAAGTCAAATTAATGATCTTAGACAA
 ACTGTCAATTTGGATGGGAGACAGGCTTGACTTAGAACATCATTTCCAGTTACAGTGTGACTGG
 AATACGTCAATTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATG
 GTTAGACGCCATCTACAGGGAAGAGAAGATAATCTCACTTTAGACATTTCCAAATTAAGAA
 CAAATTTTGAAGCATCAAAGGCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGA
 GTTGCTGATGGCCTCGCAAATCTTAACCTGTCACTTGGATTAAGACCATCAGAAGTACTATG
 ATTATAAATCTCATATTAATCGTTGTGTGCTGTTTGTCTGTTGTTAGTCTGCAGGTGTACC
 CCAACAGCTCCGAAAAAAACAGTGACATCGAGAACGGGCCATGAATGACAAAGGCGGTTTTTG
 TTCCAAAAAAAAGGGGAAATTTTGGGGAAAACCAAAAAATGAAAATGTT

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FIGURE 7D

ACA TTT GAA GTT CTA CAA TGA ACC CAT CAG AGA TGC AAA GAA AAG CGC CTC CAC GGA 57
 GAT GGT AAC ACC AGT CAC ATG GAT GGA TAA TCC TAT AGA AGT ATA TGT TAA TGA TAG 114
 M V T P V T W M D N P I E V Y V N D S 19
 TGT ATG GGT ACC TGG CCC CAC AGA TGA TCG CTG CCC TGC CAA ACC TGA GGA AGA AGG 171
 Y W V P G P T D D R C P A K P E E E G 38
 GAT GAT GAT AAA TAT TTC CAT TGG GTA TCA TTA TCC TCC TAT TTG CCT AGG GAG AGC 228
 M M I N I S I G Y H Y P P I C L G R A 57
 ACC AGG ATG TTT AAT GCC TGC AGT CCA AAA TTG GTT GGT AGA AGT ACC TAC TGT CAG 285
 P G C L M P A V Q N W L V E V P T V S 76
 TCC TAA CAG TAG ATT CAC TTA TCA CAT GGT AAG CGG GAT GTC ACT CAG GCC ACG GGT 342
 P N S R F T Y H M V S G M S L R P R V 95
 AAA TTA TTT ACA AGA CTT TTC TTA TCA AAG ATC ATT AAA ATT TAG ACC TAA AGG GAA 399
 N Y L Q D F S Y Q R S L K F R P K G K 114
 AAC TTG CCC CAA GGA AAT TCC TAA AGG ATC AAA GAA TAC AGA AGT TTT AGT TTG GGA 456
 T C P K E I P K G S K N T E V L V W E 133
 AGA ATG TGT GGC CAA TAG TGT GGT GAT ATT ACA AAA CAA TGA ATT CGG AAC TAT TAT 513
 E C V A N S V V I L Q N N E F G T I I 152
 AGA TTA G 520
 D 153

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FIGURE 7E

k1,2-22-env/fs

ACATTTGAAGTTCTACAATGAACCCATCAGAGATGCAAAGAAAAGCGCCTCCACGGAGATGGTA
ACACCAAGTCACATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGGGTACCTG
GCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTCCAT
TGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGTCCAA
AATTGGTTGGTAGAAGTACCTACTGTCAGTCCTAACAGTAGATTCACTTATCACATGGTAAGCG
GGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATT
TAGACCTAAAGGGAAAACCTTGCCCCAAGGAAATTCCTAAAGGATCAAAGAATACAGAAGTTTTA
GTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAATTCGGAACCTATTA
TAGATTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGTCGTGTCCAAG
TGCACAAGTGAGTCCAGCTGTTCGATAG

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FIGURE 7F

iddmk1,2 22-ENV

MVTPVTWMDNPIEVYVND SVWVPGPTDDRCPAKPEEEGMMINISIGYHYPPICLGRA
PGCLMPAVQNWLV E VPTVSPNSRFTYH MVSGMSLRPRVNYLQDFS YQRSLKFRPKG
KTC PK EIPK GSKNTEVLVWEECVANSV VILQNN EFGTIDZAPRGQFYHNC SGQTQSC
PSAQVSPA VDSDLTESLDKHKHKKLQSFYLWEWEEKGISTPRPKIISPVS GP EHP EL
WRLTVASHHIRIWSGNQTL ETRYRKPFYTIDLNSILTVPLQ SCLKPPYMLVVGNTVIKP
ASQTITCENCRLFTCIDSTFNWQHRILLVRAREGMWIPVSTDRPWEASPSIHILTEILK
GVLNRSKR FIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTR LWNS
QSSIDQKLASQINDLRQTVIWMGDRLDLEHHFQLQCDWNTSDFCITPQIYNESEHH
WDMVRRHLQGREDNLTLDISKLEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVT
WIKTIRSTMIINLILIVCLFCLLLVCRCTPTAPKKT VTSRTGHE

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FIGURE 7G

ACATTTGAAGTTCTACAATGAACCCATCAGAGATGCAAAGAAAAGCGCCTCCACGGAGATGGT 63
 AACACCAAGTCACATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGGGTACC 2
 T P V T W M D N P I E V Y V N D S V W V P M V 126
 TGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTC 23
 G P T D D R C P A K P E E E G M M I N I S 189
 CATTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGT 44
 I G Y H Y P P I C L G R A P G C L M P A V 252
 CCAAATTTGGTTGGTAGAAGTACCTACTGTCAGTCCTAACAGTAGATTCACTTATCACATGGT 65
 Q N W L V E V P T V S P N S R F T Y H M V 315
 AAGCGGGATGTCACTCAGGCCACGGGTAAATTATTACAGACTTTTCTTATCAAAGATCATT 86
 S G M S L R P R V N Y L Q D F S Y Q R S L 378
 AAAATTTAGACCTAAAGGGAAAACCTGCCCAAGGAAATTCCTAAAGGATCAAAGAATACAGA 107
 K F R P K G K T C P K E I P K G S K N T E 431
 AGTTTGTAGTTTCGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAATTCGG 128
 V L V W E E C V A N S V V I L O N N E F G 504
 AACTATTATAGATTTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGT 149
 T I I D L G T S R S I L P O L L R T N S V 567
 CGTGTCCAAGTGCACAAGTGAGTCCAGCTGTCTGATAG 170
 V S K C T S E S S C R 601
 181

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FIGURE 7H

iddmk1,2 22-POL

FTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVRDKFSDC
YIIHYFDDILCAAETKDKLIDCYTFLPAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQ
KIEIRKDTLKTLDNFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLT

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FIGURE 8A**k1,2-1**

gtaaatgacacctatgatgcactgccaccctttcactgtttcacccctgaacatctgctttttac
atctaagtgattgtacccaataaatagtgtggagaccagagctctgagccttttgagcctcca
ttttgcaactggteccctggctcccacctttatgaactcttaacctgtcttttctcattccttt
gtcaccattggactttgggtaccctacgggtggtggtgaggctgtcacccgcacattaa

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FIGURE 8B

k1,2-10

gttagttaatctataatctatagagacaatgcttatcactggcttgctgtcaataaatatgtg
ggtaaatctctgttcaagactctcagctttgaagctgtgagaccctgatttcccactccacac
ctctatatttctgtgtgtgtgtctttaattcctccagtgttgctgggttaggggtctcctcgacg
agctgtcgtgc

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FIGURE 8C

k1,2-16

aactcagctgctgcacagtgggtcgagcctccagagctcatgccattgcagtgggtcagagcctg
gccctcctcttcctgcatagaacctggattcaatctgtaaggtgggaagtgcagcagcagaga
actctggccttgagagagtcctctgttcccacttcactttccttttcaccaaataaaacctg
ctttcactcatgcatcaaattgtctgtgagcctacatTTTTgtggccatgggacaagaacacc
atctttagctgagctagggaaaagtcctgca

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FIGURE 8D

k1,2-17

gatgtgaccactgtgacctacctacactggagatggctcacacttccttacccttcccctgct
gtaccaataaataaacagcacagcctgacattcggagccattacgggtctttgtgacttgggtgg
tagtggtatcccctagggcccagctgtcttttcttttatctctttgtcttgtgtctttatttc
tatgagtctctcgtctccgcacatggggagaaaaacccatagaccctgtagggctg

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FIGURE 8E

x1,2-26

ctcacaaaaataataaaaagcttctgttggccattcttcagatcttcatctcttgtgaggatcc
ccctgtacatgtaaaaatgtaataaaacttgtatcctttctcctcttaatctgtcttgcac
atatcattcctagaccagtcagagatgggtggagggtgagccgtacatttccta

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FIGURE 8F

k1,2-27

cagagaactccagccagctgtgatggagcctcaggaagttcacagttgcagcaggaaggagcctggc
tgctcctcttcctgtgtggaacctgggattagaacaggctggcaggaagtgttttagcagggactct
ggcctactcacactccttgtttccccctttcttccttttcaactcaataaagccctgtcttactcac
cattcaaattgtctgtgagcctgaattttcatggctgtgggacaaagaaccctatttttagctgaac
taaggaaaattcctgcaaa

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FIGURE 8G

k1,2-4

gtgattgtctgctgaccctctccccacaattgtcttgtagaccctgacacatccccctcttcga
gaaacacccgcggatgatcaataaatattaagggaactcagaggctggcaggatcctccatat
gctgaacgctggttgccccgggtcccccttctttctttctctataactttgtctctgtgtctttt
tcttttccaaatctctcgtcccaccttacgagaaacacccacaggtgtgtccgggcaacccaa
cgccacataaca

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FIGURE 9

